Package ‘scTHI’

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Title  Identification of significantly activated ligand-receptor interactions across clusters of cells from single-cell RNA sequencing data

Version  1.16.0

Description  scTHI is an R package to identify active pairs of ligand-receptors from single cells in order to study, among others, tumor-host interactions. scTHI contains a set of signatures to classify cells from the tumor microenvironment.

Depends  R (>= 4.0)

License  GPL-2

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Suggests  scTHI.data, knitr, rmarkdown, BiocStyle

VignetteBuilder  knitr

biocViews  Software,SingleCell

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**scTHI**  
*single cell Tumor Hist Interaction (scTHI)*

**Description**

Identification of significantly activated ligand-receptor interactions across clusters of cells from single-cell RNA sequencing data. Single-cell RNA sequencing is the reference technique to characterize the heterogeneity of tumor microenvironment. The composition of the various cell types making up the microenvironment can significantly affect the way in which the immune system activates cancer rejection mechanisms. Understanding the cross-talk signals between immune cells and cancer cells is fundamental for the identification of immuno-oncology therapeutic targets. scTHI is a novel method, single cell Tumor-Host Interaction tool (scTHI), to identify significantly activated ligand-receptor interactions across clusters of cells from single-cell RNA sequencing data. scTHI is based on the hypothesis that when patterns of interaction are active, they are also simultaneously and highly expressed in homogeneous cell populations. We also model the autocrine and paracrine signalling effects of L-R partners.

**Details**

Please have a look at the vignette for a in-depth introduction to the package.

**scTHI_plotCluster**

**Description**

Graphs the output of scTHI_runTsne, labeling cells by clusters.

**Usage**

```
scTHI_plotCluster(scTHIresult, cexPoint = 0.8, legendPos = c("topleft", "topright", "bottomright", "bottomleft"))
```
Arguments

- **scTHIresult**: scTHI object.
- **cexPoint**: Set the point size.
- **legendPos**: Character string to custom the legend position.

Value

None

Examples

```r
library(scTHI.data)
data(scExample)
result <- scTHI_score(scExample,
  cellCusterA = colnames(scExample)[1:30],
  cellCusterB = colnames(scExample)[31:100],
  cellCusterAName = "ClusterA",
  cellCusterBName = "ClusterB", filterCutoff = 0,
  pvalueCutoff = 1, nPermu = 100, ncore = 8)
result <- scTHI_runTsne(result)
scTHI_plotCluster(result)
```

Description

Generates a plot on the t-SNE coordinates to show the expression levels of an interaction pair of interest. Each cell is colored according to the corresponding gene expression value.

Usage

```r
scTHI_plotPairs(scTHIresult, cexPoint = 0.8, interactionToplot)
```

Arguments

- **scTHIresult**: scTHI object.
- **cexPoint**: Set the point size.
- **interactionToplot**: Interaction pair to plot.

Value

None
Examples

```r
library(scTHI.data)
data(scExample)
result <- scTHI_score(scExample,
cellCusterA = colnames(scExample)[1:30],
cellCusterB = colnames(scExample)[31:100],
cellCusterAName = "ClusterA",
cellCusterBName = "ClusterB", filterCutoff = 0,
pvalueCutoff = 1, nPermu = 100, ncore = 8)
result <- scTHI_runTsnne(result)
scTHI_plotPairs(result, interactionToplot = "CXCL12_CD4")
```

Description

Creates barplots of scTHI_score results.

Usage

```
scTHI_plotResult(scTHIresult, cexNames = 0.8, plotType = c("score", "pair"), nRes = NULL)
```

Arguments

- `scTHIresult` scTHI object.
- `cexNames` Size of names in barplot.
- `plotType` Type of plot to be generated. Default is "score", can be also "pair". The "score" option will generate a barplot for each resulted interaction pair, representing the calculated interaction score and the related p-Value. The "pair" option will generate two barplot for each resulted interaction pair, representing the percentage of cells of each cluster expressing partnerA and partnerB gene, respectively.
- `nRes` Number of pairs to plot (all if NULL).

Value

None

Examples

```r
library(scTHI.data)
data(scExample)
result <- scTHI_score(scExample,
cellCusterA = colnames(scExample)[1:30],
cellCusterB = colnames(scExample)[31:100],
cellCusterAName = "ClusterA",
```
**scTHI_runTsne**

```r
scTHI_runTsne(scTHIresult)
```

**Arguments**

- `scTHIresult`: scTHI object.

**Value**

The same object as scTHI_score with a fifth item tsneData (data.frame)

**Examples**

```r
library(scTHI.data)
data(scExample)
result <- scTHI_score(scExample,
  cellCusterA = colnames(scExample)[1:30],
  cellCusterB = colnames(scExample)[31:100],
  cellCusterAName = "ClusterA",
  cellCusterBName = "ClusterB", filterCutoff = 0,
  pvalueCutoff = 1, nPermu = 100, ncore = 8)
result <- scTHI_runTsne(result)
```

**scTHI_score**

**Description**

This function allows the user to compute a score for a set of ligand-receptor pairs, from a single cell gene expression matrix, and detect specific Tumor-Host interactions. You must specify at least two clusters of cells (for example tumor cells and immune cells).
scTHI_score

Usage

scTHI_score(expMat, cellCusterA, cellCusterB, cellCusterAName, cellCusterBName, topRank = 10, autocrineEffect = TRUE, fileNameBase = "scTHI", filterCutoff = 0.5, PValue = TRUE, pvalueCutoff = 0.05, nPermu = 1000, ncore = 8)

Arguments

expMat  ScRNA-seq gene expression matrix where rows are genes presented with Hugo Symbols and columns are cells. Gene expression values should be counts or normalized counts.

cellCusterA  Vector of columns of expMat that belong to the first cluster.

cellCusterB  Vector of columns of expMat that belong to the second cluster.

cellCusterAName  A character string labeling the clusterA.

cellCusterBName  A character string labeling the clusterB.

topRank  Filter threshold. Set to 10 (default) means that each gene of the interaction pair will be considered as expressed in a cell if it’s in the top rank 10 percent.

autocrineEffect  if TRUE remove the paracrine filter

fileNameBase  Project name.

filterCutoff  Score threshold (default is 0.50). For each interaction pair, if the score calculated (for the partnerA or partnerB) will be less than filterCutoff the interaction pair will be discarded.

PValue  Logical, set to TRUE (default) compute statistical iterations. If p.value < 0.05, the value will be returned.

pvalueCutoff  cutoff of the p-value

nPermu  Number of iterations to perform (default is 1000).

ncore  Number of processors to use.

Value

A list of results, with four items: result (data.frame), expMat (matrix), clusterA (character), clusterB (character)

Examples

############### example of scTHI_score
library(scTHI.data)
data(scExample)
result <- scTHI_score(scExample,
cellCusterA = colnames(scExample)[1:30],
cellCusterB = colnames(scExample)[31:100],
cellCusterAName = "ClusterA",
cellCusterBName = "ClusterB", filterCutoff = 0,
**TME_classification**

\[ pvalueCutoff = 1, nPermu = 100, ncore = 8 \]

---

### Description

The function allows the user to classify non-tumor cells in tumor microenvironment. It implements the Mann-Whitney-Wilcoxon Gene Set Test (MWW-GST) algorithm and tests for each cell the enrichment of a collection of signatures of different cell types.

### Usage

```r
TME_classification(expMat, minLenGeneSet = 10,
  alternative = "two.sided", pvalFilter = FALSE, fdrFilter = TRUE,
  pvalCutoff = 0.01, nesCutoff = 0.58, nNES = 1)
```

### Arguments

- `expMat` Gene expression matrix where rows are genes presented with Hugo Symbols and columns are cells. Gene expression values should be normalized counts.
- `minLenGeneSet` Minimum gene set length
- `alternative` a character string specifying the alternative hypothesis of wilcoxon test, must be one of "two.sided" (default), "greater" or "less".
- `pvalFilter` Logical, if TRUE results will be filtered for p-Value. Default is FALSE.
- `fdrFilter` Logical, if TRUE results will be filtered for FDR.
- `pvalCutoff` Numeric p-Value (or FDR) threshold. Gene set with p-Value (or FDR) greater than pvalCutoff will be discarded (default is 0.01).
- `nesCutoff` Numeric threshold. Gene set with NES greater than nesCutoff will be discarded (default is 0.58)
- `nNES` Default is 0.58, so each cell is classified with a specific phenotype based on the first significant enriched gene set.

### Value

A list with two items: Class (character) and ClassLegend (character)

### Examples

```r
library(scTHI.data)
data(scExample)
Class <- TME_classification(scExample)
```
**TME_plot**

**Description**
Generates a plot on the t-SNE coordinates, labeling cells by TME classification.

**Usage**

```r
TME_plot(tsneData, Class, cexPoint = 0.8)
```

**Arguments**

- `tsneData`: X and y coordinates of points in the plot.
- `Class`: Object returned by `TME_classification` function.
- `cexPoint`: Set the point size.

**Value**
None

**Examples**

```r
library(scTHI.data)
data(scExample)
result <- scTHI_score(scExample,
cellCusterA = colnames(scExample)[1:30],
cellCusterB = colnames(scExample)[31:100],
cellCusterAName = "ClusterA",
cellCusterBName = "ClusterB", filterCutoff = 0,
pvalueCutoff = 1, nPermu = 100, ncore = 8)
result <- scTHI_runTsne(result)
Class <- TME_classification(scExample)
TME_plot(tsneData = result$tsneData, Class)
```
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